

Claims

1. A method for predicting the structure of a gene regulator binding site, comprising:

(a) a step for providing a gene of interest, of which a user of the method desires to predict the regulation-related structure of a binding site to which a regulator binds, the binding site being present within an enhancer or promoter region to which a protein serving as a transcriptional element is bound and which is present upstream or downstream to a coding region of the gene;

(b) a step for constructing a calculation model for each of the binding sites within the enhancer or promoter region, the binding sites being such that relevant regulators or hypothetically introduced regulators are to be bound thereto, the calculation model employing, as parameters, loci of the regulator binding sites or other factors that cause expression of the gene;

(c) a step for computing the level of transcription of the gene with respect to the above-constructed calculation model;

(d) a step for searching, through use of parameter search algorithms, parameters of the calculation model so that empirically known expression of the gene is obtained; and

(e) a step for predicting microstructures of the enhancer or promoter.

2. The method for predicting the structure of a gene

regulator binding site as described in claim 1, wherein said other factors that cause expression of the gene include temperature, molecular weight, diffusion coefficient, binding affinity, reaction rate, reverse reaction rate, and %transcription per occurrence of transcription.

3. The method for predicting the structure of a gene regulator binding site as described in claim 1 or 2, wherein, from the searched parameter sets, microstructures comprising binding sites of the enhancer or promoter, some of the binding sites interacting locally with one another, are predicted as follows:

at portions where binding sites are dense, the microstructures are physically close to one another for interaction therebetween, or they are physically remote from one another but interact with one another closely and functionally, and

at portions where binding sites are sparse, the microstructures are physically remote from one another and yet functional, or they are functionally independent from one another.

4. Apparatus for predicting the structure of a gene regulator binding site, comprising:

(a) means for providing a gene of interest, of which a user of the method desires to predict the binding site to which a regulator binds, the binding site being present within an enhancer or promoter region to which a protein is bound and which is present in an upstream or downstream

region;

(b) means for constructing a calculation model which employs, as parameters, loci of the regulator binding sites within the enhancer or promoter region or other factors that cause expression of the gene;

(c) means for computing the transcription level of the gene with respect to the above-constructed calculation model;

(d) means for searching, through use of parameter search algorithms, parameters of the calculation model so that empirically known expression of the gene is obtained; and

(e) means for predicting microstructures of the enhancer or promoter.

5. The apparatus for predicting the structure of a gene regulator binding site as described in claim 4, wherein said other factors that cause expression of the gene include temperature, molecular weight, diffusion coefficient, binding affinity, reaction rate, reverse reaction rate, and %transcription per occurrence of transcription.

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